

200

113r PKACa

1jlu_AMPK	MADVFFGN	DSTAQDVANRFARGALRQKRNVEBVKHKEIARFFKQPTIFCSHCDDFI	GFKQGFOCOVCFCVVHKRCHEFVTSSCPAGDKGEPDTD	DPRSKHKFKIHTYGSPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
PKCa.h	MADVYFAN	DSTAQDVANRFARGALRQKRNVEBVKHKEIARFFKQPTIFCSHCDDFI	GFKQGFOCOVCFCVVHKRCHEFVTSSCPAGDKGEPDTD	DPRSKHKFKIHTYGSPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
6755078.m	MADVYFAA	EPAAPODVANRFARGALRQKRNVEBVKHKEIARFFKQPTIFCSHCDDFI	GFKQGFOCOVCFCVVHKRCHEFVTSSCPAGDKGEPDTD	DPRSKHKFKIHTYGSPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
27806089.m	MGLKLKRTHAHERI	QVRDARPVVLVAIKNGECPVYASGGCPTTLISPMTQVQIVVRSRRHSECGCA	VSTQTFLVIVMEWSLWEVKEMKPSKCSDDHIIWATLKLFLFIITIVPVIVV	DPRSKHKFKIHTYGSPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
34874121.m	MADPAAGP	PPSEGEESTVRFARGALRQKRNVEBVKRNHEKETARFFKQPTIFCSHCDDFI	GFKQGFOCOVCFCVVHKRCHEFVTSSCPAGDKGEPASD	DPRSKHKFKIHTYGSPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
6679345.m	MADPAAGP	PPSEGEESTVRFARGALRQKRNVEBVKRNHEKETARFFKQPTIFCSHCDDFI	GFKQGFOCOVCFCVVHKRCHEFVTSSCPAGDKGEPASD	DPRSKHKFKIHTYGSPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
PKCb.h	MADPAAGP	PPSEGEESTVRFARGALRQKRNVEBVKRNHEKETARFFKQPTIFCSHCDDFI	GFKQGFOCOVCFCVVHKRCHEFVTSSCPAGDKGEPASD	DPRSKHKFKIHTYGSPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
27807061.m	MADPAAGP	PPSEGEESTVRFARGALRQKRNVEBVKRNHEKETARFFKQPTIFCSHCDDFI	GFKQGFOCOVCFCVVHKRCHEFVTSSCPAGDKGEPASD	DPRSKHKFKIHTYGSPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
6981398.m	MADPAAGP	PPSEGEESTVRFARGALRQKRNVEBVKRNHEKETARFFKQPTIFCSHCDDFI	GFKQGFOCOVCFCVVHKRCHEFVTSSCPAGDKGEPASD	DPRSKHKFKIHTYGSPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
6755080.m	MAGLGPGGG	GDSEGPP_RPLFCRKALRQKRNVEBVKRNHEKETARFFKQPTIFCSHCDDFI	IKGQKQOCOVCFCVVHRRKCHEFVTECFCAGAKGQPTD	DPRSKHKFKIHTYGSPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
6981400.m	MAGLGPGGG	GDSEGPP_RPLFCRKALRQKRNVEBVKRNHEKETARFFKQPTIFCSHCDDFI	IKGQKQOCOVCFCVVHRRKCHEFVTECFCAGAKGQPTD	DPRSKHKFKIHTYGSPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
PKCg.h	MAGLGPGV	GDSEGPP_RPLFCRKALRQKRNVEBVKRNHEKETARFFKQPTIFCSHCDDFI	IKGQKQOCOVCFCVVHRRKCHEFVTECFCAGAKGQPTD	DPRSKHKFKIHTYGSPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
32566197.w	MELSTINSSVK	EDEAQRIEGKAFAVRGALRQKRNVEBVKHKEIARFFKQPTIFCSHCDDFI	INKQKQOCOVCFCVVHKRCHEFVNACBGADKGVDTD	DPRQHOKWQVOTYSSEPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
25146870.w	MELSTINSSVK	EDEAQRIEGKAFAVRGALRQKRNVEBVKHKEIARFFKQPTIFCSHCDDFI	INKQKQOCOVCFCVVHKRCHEFVNACBGADKGVDTD	DPRQHOKWQVOTYSSEPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
24654282.f	MSEGSDNNGPQQQGAE	GEAVGENKMSKSLRKAGAKKKNNVNVKHDICARFFKQPTIFCSHCDDFI	GQYSGQSYAWMGFGKQGFOCOVCFCVVHKRCHEFVTCFCAGDKGKEDSD	SPHQONFEEFPTVTAFCPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
171336402.f	MSEGSDNNGPQQQGAE	GEAVGENKMSKSLRKAGAKKKNNVNVKHDICARFFKQPTIFCSHCDDFI	GKQGFOCOVCFCVVHKRCHEFVTCFCAGDKGKEDSD	SPHQONFEEFPTVTAFCPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
31239753.i				DPRSKHKFKIHTYGSPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
17136716.f	MAAAAATPGATVLPSSVPSSAAPGAKAPAAGAGKPGPNLLEITGEANIVNYMKNRLRKGAMKRKSL	EVNCHRSGVRFKPTYCHRKDFP	FKQGFOCOVCFCVVHKRCHEFVTECFCAGDKGADSD	CAGVKHSVISTTYTPTFCDCHGCGSLLYLIIHOGCKMCD1CDMNVIKRC
1muo_AUR1				
1lomy_GPRK2			MADLEAVLADVSYLMAMEKSKATPAARASKKILLPEPS	IRSVMQKYLEDRSEVTFERESKQLG

400

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600

11.2 - DWG

Sequence logo showing the conservation of amino acids across 100 protein sequences from positions 610 to 920. The x-axis represents positions 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, and 920. The y-axis lists 113 sequences. Each sequence is represented by a vertical bar where each segment's color corresponds to a different amino acid. A legend at the bottom indicates the color coding for each amino acid.